

AMENDMENT TO THE CLAIMS

Please cancel Claims 2-11 without prejudice and amend Claims 1, 22, 32, 33 and 38 as shown in the following listing of the claims:

1. (Currently amended) A method for determining whether a human immunodeficiency virus type 1 (HIV-1) has an increased likelihood of having a reduced susceptibility to treatment with ~~a protease inhibitor~~ amprenavir, comprising: detecting whether the protease encoded by said HIV-1 exhibits the presence or absence of a mutation associated with reduced susceptibility to treatment with said protease inhibitor at amino acid position 11, 32, 33, 34, 43, 46, 47, 48, 50, 54, 58, 71, 76, 79, 82, 83, 84, 91 or 95 of an amino acid sequence of said protease, wherein the presence of said mutation indicates that the HIV-1 has an increased likelihood of having reduced susceptibility to treatment with ~~the protease inhibitor~~ amprenavir, with the proviso that said mutation is not V32I, M46I, M46L, I47V, I50V, I54L, I54M, I54V, V82A or I84V.
- 2.-11. (Canceled)
12. (Original) The method of claim 1, wherein the amino acid at position 11, 33, 43, 48, 54, 71, 76, 82, 84, 91 or 95 of said protease is an amino acid having a neutral, hydrophobic or non-polar side chain.
13. (Original) The method of claim 12, wherein the amino acid at position 11 of said protease is I or L.
14. (Original) The method of claim 12, wherein the amino acid at position 33 of said protease is F.
15. (Original) The method of claim 1, wherein the amino acid at position 34 of said protease is an amino acid having a neutral, polar or hydrophilic side chain.
16. (Original) The method of claim 15, wherein the amino acid at position 34 of said protease is Q.
17. (Original) The method of claim 12, wherein the amino acid at position 43 of said protease is T.

18. (Original) The method of claim 12, wherein the amino acid at position 48 of said protease is M.
19. (Original) The method of claim 12, wherein the amino acid at position 54 of said protease is A.
20. (Original) The method of claim 12, wherein the amino acid at position 71 of said protease is L.
21. (Original) The method of claim 12, wherein the amino acid at position 76 of said protease is V.
22. (Currently Amended) The method of claim 12, wherein the amino acid at position 82 of said protease is A or F.
23. (Original) The method of claim 12, wherein the amino acid at position 84 of said protease is A.
24. (Original) The method of claim 12, wherein the amino acid at position 91 of said protease is A or V.
25. (Original) The method of claim 12, wherein the amino acid at position 95 of said protease is F.
26. (Original) The method of claim 1, wherein the amino acid at position 54 of said protease is an amino acid with a neutral, hydrophobic, non-polar, hydrophilic or polar side chain.
27. (Original) The method of claim 1, wherein the amino acid at position 54 of said protease is an amino acid with a neutral, hydrophilic or polar side chain.
28. (Original) The method of claim 27, wherein the amino acid at position 54 of said protease is S or T.
29. (Original) The method of claim 1, wherein the amino acid at position 58 or 83 of said protease is an amino acid with an acidic, hydrophilic or polar side chain.

30. (Original) The method of claim 29, wherein the amino acid at position 58 of said protease is E.
31. (Original) The method of claim 1, wherein the amino acid at position 83 of said protease is D.
32. (Currently amended) The method of claim 1, wherein the amino acid at position 79 of said protease is an amino acid with a neutral, hydrophobic, non-polar, acidic, hydrophilic or polar side chain, with the proviso that the amino acid at position 79 is not P.
33. (Currently amended) The method of claim 1, wherein the amino acid at position 79 of said protease is an amino acid with a neutral, hydrophobic or non-polar side chain, with the proviso that the amino acid at position 79 is not P.
34. (Original) The method of claim 1, wherein the amino acid at position 79 of said protease is an amino acid with an acidic, neutral, hydrophilic or polar side chain.
35. (Original) The method of claim 1, wherein the amino acid at position 79 of said protease is any amino acid, with the proviso that it is not P.
36. (Original) The method of claim 1, wherein the amino acid at position 84 of said protease is an amino acid with a neutral, hydrophobic, non-polar, hydrophilic or polar side chain.
37. (Original) The method of claim 1, wherein the amino acid at position 84 of said protease is an amino acid with a neutral, hydrophilic or polar side chain.
38. (Currently amended) The method of claim 38 37, wherein the amino acid at position 84 of said protease is C.
39. (Original) The method of claim 1, wherein the amino acid at position 91 of said protease is an amino acid with a neutral, hydrophobic, non-polar, hydrophilic or polar side chain.

40. (Original) The method of claim 1, wherein the amino acid at position 91 of said protease is an amino acid with a neutral, hydrophilic or polar side chain.
41. (Original) The method of claim 40, wherein the amino acid at position 91 of said protease is S.
42. (Original) The method of claim 1, wherein the method comprises detecting the presence or absence of a mutation associated with reduced susceptibility to treatment with said protease inhibitor at at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 or 19 of the amino acid positions.